RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/728,420 A*

Source: *1 Fwo*

Date Processed by STIC: *8/13/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

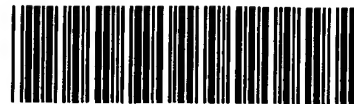http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

IFWO

RAW SEQUENCE LISTING   DATE: 08/13/2004
PATENT APPLICATION: US/10/728,420A   TIME: 16:13:54

Input Set : **D:\Sequence Listing-rev.txt**
Output Set: **N:\CRF4\08132004\J728420A.raw**

```
   4 <110> APPLICANT: WOULFE, SUSAN L.
   5        JAIN, RITA
   6        BURR, AIMEE
   8 <120> TITLE OF INVENTION: ENGINEERED FAB' FRAGMENT ANTI-TUMOR
   9        NECROSIS FACTOR ALPHA IN COMBINATION WITH DISEASE MODIFYING
  10        ANTI-RHEUMATIC DRUGS
  12 <130> FILE REFERENCE: 122294-1010
  14 <140> CURRENT APPLICATION NUMBER: US/10/728,420A
  16 <141> CURRENT FILING DATE: 2003-12-05
  18 <150> PRIOR APPLICATION NUMBER: US 60/431,053
  20 <151> PRIOR FILING DATE: 2002-12-05
E--> 22 <160> NUMBER OF SEQ ID NOS: (40) 117 (p.2)
  24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
E--> 389 <210> SEQ ID NO: 46
```
(see p.3)

Does Not Comply
Corrected Diskette Needed

<210> 117 *Last sequence in submitted*
                        file
<211> 1477
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic CDP870 nucleic acid sequence (anti-sense strand)

<400> 117
tcatcacgcg gcgcatgtgt gagttttgtc acaagatttg ggctcaactt tcttgtggac 60
cttggtgttg ctgggcttgt gattcacgtt gcagatgtag gtctgggtgc ccaagctgct 120
ggagggcacg gtcaccacgc tgctgaggga gtagagtcct gaggactgta ggacagccgg 180
gaaggtgtgc acgccgctgg tcagggcgcc tgagttccac gacaccgtca ccggttcggg 240
gaagtagtcc ttgaccaggc agcccaggyc cgctgtgccc ccagaggtgc tcttggagga 300
gggtgccagg gggaagaccg atgggccctt ggtggaagct gaggagactg tgactagggt 360
accctggccc cagtagtcca tggcataaga tctgtatcct ctagcacaat agtacactgc 420
ggtgtcctct gctctcaggc tattcatttg gaggtatgct gttgacttgg atgtgtctag 480
agagaacgtg aatctcgcct tgacgctgtc agcataaata ggctctccaa tgtaagtatt 540
aatccaaccc atccattcga ggcccttttcc cggggcctgt ctaacccaat tcattccata 600
gtctgtgaag acgtaaccag atgcagcaca ggacaatctc agtgatccgc caggctgcac 660
gagaccgcct cctgactcga ccagctgaac ctcagcttgc gccacggtgg cgaaaccagc 720
tagcgccact gcaattgcta tagcagtttt cttcattttt ttttcctcct caacactctc 780
ctctattaaa gcttttgtt actggtgagc tcaggccctg atgggtgact tcgcaggcgt 840
aagctttgtg tttctcgtag tctgctttcc tcagcgtcag ggtgctgctg aggctgtagg 900
tgctgtcctt gctgtcctgc tctgtgacac tctcctggga gttacccgat tggagggcgt 960
tatccacctt ccactgtact ttggcctctc tgggatagaa gttattcagc aggcacacaa 1020
cagaggcagt tccagatttc aactgctcat cagatggcgg gaagatgaag acagatgggg 1080
ccgctaccgt acgtttgatt tctactttag taccctgacc gaatgtgagt gggtagatgt 1140
tatactgttg acagtaataa gtggcgaaat cttctggctg gaggctacta gtcgtgaggg 1200
tgaaatcagt accactaccg gatccgctga acctgtatgg tacaccacta tagaggaaag 1260
aggcactgta gatgagggct tttggggctt tacctggttt ttgctgatac caggctacgt 1320
tagtacctac gttctgactg gctttacaag tgatggtgac ccggtctcct acagatgcgc 1380
tcaggctgga tgggctctgg gtcatttgaa tgtcagcttg cgctacggta gcgaaccag 1440
ccaaggccac tgcaattgcg atagctgtct ttttcat
                                                                1477

replace with

<4007

<210> 46
<210> 46
000

10/728,420A 3

L:162 M:283 W: Missing Blank Line separator, <400> field identifier
L:163 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:168 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:219 M:283 W: Missing Blank Line separator, <400> field identifier
L:220 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:224 M:283 W: Missing Blank Line separator, <400> field identifier
L:225 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:229 M:283 W: Missing Blank Line separator, <400> field identifier
L:230 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:234 M:283 W: Missing Blank Line separator, <400> field identifier
L:235 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:239 M:283 W: Missing Blank Line separator, <400> field identifier
L:240 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:244 M:283 W: Missing Blank Line separator, <400> field identifier
L:245 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:249 M:283 W: Missing Blank Line separator, <400> field identifier
L:250 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:254 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:259 M:283 W: Missing Blank Line separator, <400> field identifier
L:260 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:264 M:283 W: Missing Blank Line separator, <400> field identifier
L:265 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (21) SEQUENCE:
L:269 M:283 W: Missing Blank Line separator, <400> field identifier
L:270 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (22) SEQUENCE:
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:275 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (23) SEQUENCE:
L:279 M:283 W: Missing Blank Line separator, <400> field identifier
L:280 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (24) SEQUENCE:
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
L:285 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE:
L:289 M:283 W: Missing Blank Line separator, <400> field identifier
L:290 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (26) SEQUENCE:
L:294 M:283 W: Missing Blank Line separator, <400> field identifier
L:295 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (27) SEQUENCE:
L:299 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (28) SEQUENCE:
L:304 M:283 W: Missing Blank Line separator, <400> field identifier
L:305 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (29) SEQUENCE:
L:309 M:283 W: Missing Blank Line separator, <400> field identifier
L:310 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:315 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (31) SEQUENCE:
L:319 M:283 W: Missing Blank Line separator, <400> field identifier
L:320 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (32) SEQUENCE:
L:324 M:283 W: Missing Blank Line separator, <400> field identifier

```
L:325 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (33) SEQUENCE:
L:329 M:283 W: Missing Blank Line separator, <400> field identifier
L:330 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (34) SEQUENCE:
L:334 M:283 W: Missing Blank Line separator, <400> field identifier
L:335 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (35) SEQUENCE:
L:339 M:283 W: Missing Blank Line separator, <400> field identifier
L:340 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (36) SEQUENCE:
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:345 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (37) SEQUENCE:
L:349 M:283 W: Missing Blank Line separator, <400> field identifier
L:350 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (38) SEQUENCE:
L:354 M:283 W: Missing Blank Line separator, <400> field identifier
L:355 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:
L:359 M:283 W: Missing Blank Line separator, <400> field identifier
L:360 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (40) SEQUENCE:
L:364 M:283 W: Missing Blank Line separator, <400> field identifier
L:365 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (41) SEQUENCE:
L:369 M:283 W: Missing Blank Line separator, <400> field identifier
L:370 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (42) SEQUENCE:
L:374 M:283 W: Missing Blank Line separator, <400> field identifier
L:375 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:379 M:283 W: Missing Blank Line separator, <400> field identifier
L:380 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:384 M:283 W: Missing Blank Line separator, <400> field identifier
L:385 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:
L:389 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:46
L:389 M:283 W: Missing Blank Line separator, <210> field identifier
L:390 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:394 M:283 W: Missing Blank Line separator, <400> field identifier
L:395 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:
L:399 M:283 W: Missing Blank Line separator, <400> field identifier
L:400 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
L:404 M:283 W: Missing Blank Line separator, <400> field identifier
L:405 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
L:409 M:283 W: Missing Blank Line separator, <400> field identifier
L:410 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
L:414 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (51) SEQUENCE:
L:419 M:283 W: Missing Blank Line separator, <400> field identifier
L:420 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (52) SEQUENCE:
L:424 M:283 W: Missing Blank Line separator, <400> field identifier
L:425 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (53) SEQUENCE:
L:429 M:283 W: Missing Blank Line separator, <400> field identifier
L:430 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (54) SEQUENCE:
L:434 M:283 W: Missing Blank Line separator, <400> field identifier
L:435 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (55) SEQUENCE:
L:439 M:283 W: Missing Blank Line separator, <400> field identifier
L:440 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (56) SEQUENCE:
L:444 M:283 W: Missing Blank Line separator, <400> field identifier
```

```
L:445 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (57) SEQUENCE:
L:449 M:283 W: Missing Blank Line separator, <400> field identifier
L:450 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (58) SEQUENCE:
L:454 M:283 W: Missing Blank Line separator, <400> field identifier
L:455 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (59) SEQUENCE:
L:460 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (60) SEQUENCE:
L:890 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:894 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:101
L:913 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:102
L:937 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:103
L:961 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:104
L:985 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:105
L:22 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (40) Counted (116)
```